

SEQUENCE LISTING

GENERAL INFORMATION

(i) APPLICANT: Yelton, Dale E. Rosok, Mae Joanne

(ii) TITLE OF THE INVENTION: A METHOD FOR INHIBITING IMMUNOGLOBULIN-INDUCED

TOXICITY RESULTING FROM THE USE OF IMMUNOGLOBULINS IN THERAPY AND IN VIVO DIAGNOSIS

- (iii) NUMBER OF SEQUENCES: 29
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Bristol-Myers Squibb Company
 - (B) STREET: P.O. Box 4000
 - (C) CITY: Princeton
 - (D) STATE: NJ
 - (E) COUNTRY: USA
 - (F) ZIP: 08543
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: CD-ROM
 - (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: WINDOWS.
- ·····(D) SOFTWARE: PatentIn
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/905,293
 - (B) FILING DATE: 01-AUG-1997
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/023,033
 - (B) FILING DATE: 02-AUG-1996
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Carey, Brian
 - (B) REGISTRATION NUMBER: 44,590
 - (C) REFERENCE/DOCKET NUMBER: ON0146A
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 609-252-3883
 - (B) TELEFAX: 609-252-4526
 - (C) TELEX:
 - (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid

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(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:	
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(2) INFORMATION FOR SEQ ID NO:2:	-
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 57 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
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(2) INFORMATION FOR SEQ ID NO:3:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 55 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
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(2) INFORMATION FOR SEQ ID NO:4:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 30 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
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(2) INFORMATION FOR SEQ ID NO:5:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 36 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
ACCATGGTCG ACCTCAGACC TGCCAAGAGC CATATC	36
(2) INFORMATION FOR SEQ ID NO:6:	
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(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
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(2) INFORMATION FOR SEQ ID NO:7:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 49 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single - (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
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(2) INFORMATION FOR SEQ ID NO:8:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 50 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
GGAAAGAACC ATCACAGTCT CGCAGGGGCC CAGGGCAGCG CTGGGTGCTT	50
(2) INFORMATION FOR SEQ ID NO:9:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 8691 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

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Т	GCTCCCTGC	TTGTGTGTTG	GAGGTCGCTG	AGTAGTGCGC	GAGCAAAATT	TAAGCTACAA	240	
С	AAGGCAAGG	CTTGACCGAC	AATTGCATGA	AGAATCTGCT	TAGGGTTAGG	CGTTTTGCGC	300	
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			GCTTACTGGG				1500	
			GTCTTCCCCC				1560	The second second second
			CTGGTCAAGG				1,620	
			AGCGGCGTGC				1680	and the
			GTGGTCACCG				1740	
			AAGCCCAGCA				1800	*
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			AGTCCAGGGC				1920	
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			AGGTGCCCCT				2040	
			GAGCCATATC				2100	
			ACTCCCTCAG				2160	
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			CCAGGCCTCG				2280	
			ACAGGCCCCA				2340	
			TGGGGGGACC				2400	
			GGACCCCTGA				2460	
			TCAACTGGTA				2520	
_			AGTACAACAG				2580	
			ATGGCAAGGA				2640	
			CCATCTCCAA				2700	
			CTCGGCCCAC				2760	
			CCCCGAGAAC				2820	
			GTCAGCCTGA				2880	
			AGCAATGGGC				2940	
			TCCTTCTTCC				3000	
			TTCTCATGCT				3060	
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    CTACCCCAC GGCACTAACC CCTGGCTGCC CTGCCCAGCC TCGCACCCGC ATGGGGACAC
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    GCCTTAAGAC TTATTGAACA ACCGGAATTG GCAAGTAAAG TAGACATGGT TTGGATAGTC
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 CAGTGGAACG AAAACTCACG TTAAGGGATT TTGGTCATGA GATTATCAAA AAGGATCTTC
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GCAGTGTTAT CACTCATGGT TATGGCAGCA CTGCATAATT CTCTTACTGT CATGCCATCC
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-GTAAGATGCT TTTCTGTGAC TGGTGAGTAC TGAACCAAGT CATTCTGAGA ATAGTGTATG 8280 - **
 CGGCGACCGA GTTGCTCTTG CCCGGCGTCA ATACGGGATA ATACCGCGCC ACATAGCAGA
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                                                                     8400 .
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 TTTACTTTCA CCAGCGTTTC TGGGTGAGCA AAAACAGGAA GGCAAAATGC CGCAAAAAAG
                                                                     8520
 GGAATAAGGG CGACACGGAA ATGTTGAATA CTCATACTCT TCCTTTTTCA ATATTATTGA
                                                                     8580
 AGCATTTATC AGGGTTATTG TCTCATGAGC GGATACATAT TTGAATGTAT TTAGAAAAAT
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(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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TGCTCCCTGC	TTGTGTGTTG	GAGGTCGCTG	AGTAGTGCGC	GAGCAAAATT	TAAGCTACAA	240
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   AGGTCTCGAG TCTCTAGATA ACCGGTCAAT CGATTGGAAT TCTTGCGGCC GCTTGCTAGC
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(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8897 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

.. (ii) MOLECULE TYPE: cDNA

* I was a second of the control of t

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									- 60-
	-							-CCTGTTAGGC	
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: : : ·								TCTAGTCAGA	
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  AAGCTATGCA TTTTTATAAG ACCATGGGAC TTTTGCTGGC TTTAGATCTC TTTGTGAAGG
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  AACCTTACTT CTGTGGTGTG ACATAATTGG ACAAACTACC TACAGAGATT TAAAGCTCTA
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  CTCAACATTC TACTCCTCCA AAAAAGAAGA GAAAGGTAGA AGACCCCAAG GACTTTCCTT
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(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

					CTAGATAACC					
					TGGTTAAGCT					
					GTGGAGTCTG					
					TCTGGATTCC					
•					CTGGAGTGGG					
					AAGGGTCGAT					
The state of the s	CAGAGACAAT	GCAAAGAACA	GCCTGTACCT	GCAAATGAAC	AGCCTGAGGG	ACGAGGACAC		2 f. f. f	The Galt #1 and	± ^{yr} + ± −
المستهدلات والماسا	AGCCGTGTAT	·TACTGTGCAA	GAGGECTGGC	GGACGGGGCC	TGGTTTGCTT	AGTGGGGCCA	480		a tha a saile dheegay a sail (g	dia men
					CCATCGGTCT					•3:
					GGCTGCCTGG					
					-CTGACCAGCG					
					AGCAGCGTGG					
	CTCCAGCAGC	\cdot TTGGGCACCC	AGACCTACAT	CTGCAACGTG	AATCACAAGC	CCAGCAACAC	780			
	- CAAGGTGGAC	AAGAAAGTTG	GTGAGAGGCC	AGCACAGGGA	GGGAGGGTGT	CTGCTGGAAG		. • •		`- '
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					CGCCCCACTC					
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(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8897 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

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		TGTTGGAGGT				240	
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		GGGCCAGATA				360	
		GGTCATTAGT				420	
		CGCCTGGCTG				480	
		TAGTAACGCC				540	
		CCCACTTGGC				600	
		ACGGTAAATG				660	·
		GGCAGTACAT				720	
		TCAATGGGCG				780	
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		CCGCCCCATT				900	
		CTCTCTGGCT				960	
CGAAATTAAT	ACGACTCACT	ATAGGGAGAC	CCAAGCTTGG	TACCAATTTA	AATTGATATC	1020	-
TCCTTAGGTC	TCGAGCACCA	TGAAGTTGCC	TGTTAGGCTG	TTGGTGCTGA	TGTTCTGGAT	1080	
TCCTGCTTCC	AGCAGTGATG	TTGTCATGAC	CCAAACCCCA	CTGTCCAGTC	CTGTCACGCT	1140	
TGGACAACCT	GCGTCCATCT	CTTGCAGATC	TAGTCAGATC	ATTGTACATA	ATAATGGCAA	1200	•
CACCTATCTG	GAATGGTACC	AGCAGAGACC	AGGGCAGTCT	CCACGGCTCC	TGATCTACAA	1260	٨
AGTTTCCAAC	CGATTTTCTG	GGGTCCCAGA	CAGGTTCAGC	GGCAGTGGAG	CTGGGACAGA	1320	
TTTCACACTC	AAGATCAGCA	GAGTGGAGGC	TGAGGATGTG	GGAGTTTACT	ACTGCTTCCA	1380	·
GGGTTCACAT	GTTCCATTCA	CGTTCGGCCA	AGGGACAAAG	TTGGAAATCA	AACGTAAGTC	1440	•
TCGAGTCTCT	AGATAACCGG	TCAATCGATT	GGAATTCTAA	ACTCTGAGGG	GGTCGGATGA.	1500	a
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ACAACACACCC AGGAACTGTG TGGAACTGCC GTGGAAGGTG GAGCAAGGAC GAAACACAAA GAGCTTCAAC	GGGATAAGCA CAAGGGCAGA GCTGCACCAT TCTGTTGTGT GATAACGCCC AGCACCTACA GTCTACGCCT AGGGGAGAGT	TGCTGTTTTC ACTTTGTTAC CTGTCTTCAT GCCTGCTGAA TCCAATCGGG GCCTCAGCAG GCGAAGTCAC GTTAGAGGGA	TGTCTGTCCC TTAAACACCA CTTCCCGCCA TAACTTCTAT TAACTCCCAG CACCCTGACG CCATCAGGCC GAAGTGCCCC	TAACATGCCC TCCTGTTTGC TCTGATGAGC CCCAGAGAGG GAGAGTGTCA CTGAGCAAAG CTGAGCTCGC CACCTGCTCC	TTATCCGCAA TTCTTTCCTC AGTTGAAATC CCAAAGTACA CAGAGCAGGA CAGACTACGA CCGTCACAAA TCAGTTCCAG	1800 1860 1920 1980 2040 2100 2160	
ACAACACACCC AGGAACTGTG TGGAACTGCC GTGGAAGGTG GAGCAAGGAC GAAACACAAA GAGCTTCAAC CCTGACCCCC	GGGATAAGCA CAAGGGCAGA GCTGCACCAT TCTGTTGTGT GATAACGCCC AGCACCTACA GTCTACGCCT AGGGGAGAGT TCCCATCCTT	TGCTGTTTTC ACTTGTTAC CTGTCTTCAT GCCTGCTGAA TCCAATCGGG GCCTCAGCAG GCGAAGTCAC GTTAGAGGGA TGGCCTCTGA	TGTCTGTCCC TTAAACACCA CTTCCCGCCA TAACTTCTAT TAACTCCCAG CACCCTGACG CCATCAGGGC GAAGTGCCCC CCCTTTTTCC	TAACATGCCC TCCTGTTTGC TCTGATGAGC CCCAGAGAGG GAGAGTGTCA CTGAGCAAAG CTGAGCTCGC CACCTGCTCC ACAGGGGACC	TTATCCGCAA TTCTTTCCTC AGTTGAAATC CCAAAGTACA CAGAGCAGGA CAGACTACGA CCGTCACAAA TCAGTTCCAG TACCCCTATT	1800 1860 1920 1980 2040 2100 2160	
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ACAACACACCC AGGAACTGTG TGGAACTGCC GTGGAAGGAC GAAACACAAA GAGCTTCAAC CCTGACCCCC GCGGTCCTCC AATGTTGGAG TCATTTAATA AATATGTAGT CCCTGGGCC TAGTCCTTT AATCAACCAA AACATGATAT TTTAAGTTCA CAGGTACTGA TAATCCACAC	GGGATAAGCA CAAGGGCAGA GCTGCACCAT TCTGTTGTTGT GATAACGCCC AGCACCTACA GTCTACGCCT AGGGGAGAGT TCCCATCCTT AGCTCATCTT GAGAATGAAT ATTATTATCT CATCCTAAGG CTCTGCAAGA ATGGTAGGAG TAAGGGTGAC AGCAAATTTT AAATAACAA TCATGGTACT GGGACTCCTG TATACTGTA	TGCTGTTTCC ACTTGTTAC CTGTCTCAT GCCTGCTGAA TCCAATCGGG GCCTCAGCAG GCGAAGTCAC GTTAGAGGGA TCACCTCACC	TGTCTGTCCC TTAAACACCA CTTCCCGCCA TAACTTCTAT TAACTCCAG CACCTGACG CACCTGACG CATCAGGGC GAAGTGCCCC CCCTTTTTCC CCCTCCTCC AATCTTTGCA CAACTACTCA TTATAAAAA TCAAACCCAC CCTTGTTTC GTCATATAT GAATTCATAAAT GGAATGTCAT GCCGTATTGA ATTCATTAAA	TAACATGCCC TCCTGTTTGC TCTGATGAGC CCCAGAGAGG GAGAGTGTCA CTGAGCAAAG CTGAGCTCGC CACCTGCTCC ACAGGGGACC TCCTTGGCTT CCTGTGGTTT ATTTCTCTTA TCATCCTTCA AAGCCTTCTG CCTCCTCAG CTTTGATTCA TAAAGAGAAT AAACAAACAA GCCTTATTTA GTACTTTCCA ATGTTGCAAA	TTATCCGCAA TTCTTTCCTC AGTTGAAATC CCAAAGTACA CAGAGCAGGA CAGACTACGA CCGTCACAAA TCAGTTCCAG TACCCCTATT TAATTATGCT CTCTCTTTCC TAAGGGACTA TCCTCACAGT CAAGCCCTCA ATTCCCTGAG CATTCATTGC TAGGGAAATG CATTCATTTAAA CAACCTAATT GGTTCTATAA	1800- 1860 1920 1980 2040 2100 2160 2220 2280 2340 2400 2460 2520 2580 2640 2700 2760 2820 2880	
ACAACACACCC AGGAACTGTG TGGAACTGCC GTGGAAGGAC GAAACACAAA GAGCTTCAAC CCTGACCCCC GCGGTCCTCC AATGTTGGAG TCATTTAATA AATATGTAGT CCCTGGGCC TAGTCCTTT AATCAACCAA AACATGATAT TTTAAGTTCA CAGGTACTGA TAATCCACAC AGCTGAGAGA	GGGATAAGCA CAAGGGCAGA GCTGCACCAT TCTGTTGTTGT GATAACGCCC AGCACCTACA GTCTACGCCT AGGGGAGAGT TCCCATCCTT AGCTCATCTT GAGAATGAAT ATTATTATCT CATCCTAAGG CTCTGCAAGA ATGGTAGGAG ATGGTAGGAC AGCAAATTTT AAATAACAA TCATGGTACT GGGACTCCTG TATACTGTGA CAAATATTT	TGCTGTTTCC ACTTGTTAC CTGTCTCAT GCCTGCTGAA TCCAATCGGG GCCTCAGCAG GCGAAGTCAC GTTAGAGGGA TCACCTCACC	TTTTTCCC TTTAAACACCA TTAACTCCAG TAACTTCTAT TAACTCCAG CACCTGACG CATCAGGGC GAAGTGCCCC CCCTTTTTCC CCCTCCTCC AATCTTTGCA CAACTACTCA TTTATAAAAA TCAAACCCAC CCTTGTTTC GTCATATTC AAACCTGCTA GCAATTAAAT GGAATGTCAT GCCGTATTGA ATTCATTAAA ACCGCTATTGA ATTCATTAAA GCAATCCCAC	TAACATGCCC TCCTGTTTGC TCTGATGAGC CCCAGAGAGG GAGAGTGTCA CTGAGCAAAG CTGAGCTCGC CACCTGCTCC ACAGGGGACC TCCTTGGCTT CCTGTGGTTT ATTTCTCTTA TCATCCTTCA AAGCCTTCTG CCTCCTCAG CTTTGATTCA TAAAGAGAAT AAACAAACAA GCCTTATTTA GTACTTTCCA ATGTTGCAAA TTCTAGATGA	TTATCCGCAA TTCTTTCCTC AGTTGAAATC CCAAAGTACA CAGAGCAGA CAGACTACGA CCGTCACAAA TCAGTTCCAG TACCCCTATT TAATTATGCT CTCTCTTTCC TAAGGGACTA TCTATTTTA TCCTCACAGT CAAGCCCTCA ATTCCCTGAG CATTCATTGC TAGGGAAATG CATTCATTTAAA CAACCTAATT GGTTCTATAAA CTGAGTGCCC	1740- 1800- 1860- 1920- 1980- 2040- 2160- 2220- 2280- 2340- 2460- 2520- 2580- 2640- 2760- 2820- 2820- 2880- 2940-	
ACAACACACCCAGGAACTGTG TGGAACTGCC GTGGAAGGAC GAACACAAA GAGCTTCAAC CCTGACCCCC GCGGTCCTCC AATGTTGGAG TCATTTAATA AATATGTAGT CCCTATCATC CCCCTGGCCC TAGTCCTTT AATCAACCAA AACATGATAT TTTAAGTTCA CAGGTACTGA CAGGTACTGA TAATCCACAC AGCTGAGAGA CCACCCACCA	GGGATAAGCA CAAGGGCAGA GCTGCACCAT TCTGTTGTGT GATAACGCCC AGCACCTACA GTCTACGCCT AGGGGAGAGT TCCCATCCTT AGCTCATCTT GAGAATGAAT ATTATTATCT CATCCTAAGG CTCTGCAAGA ATGGTAGGAG TAAGGGTGAC AGCAAATTTT AAAATAACAA TCATGGTACT GGGACTCCTG TATACTGTGA CAAATATTT AAAAAACTATG	TGCTGTTTCC TGTCTTCAT GCCTGCTGAA TCCAATCGGG GCCTCAGCAG GCGAAGTCAC GTTAGAGGGA TCACCTCACC	ETGTCTGTCCC TTAAACACCA CTTCCCGCCA TAACTTCTAT TAACTCCAG CACCTGACG CATCAGGGC GAAGTGCCCC CCCTTTTTCC CCCTCCTCC AATCTTTGCA CAACTACTCA TTATAAAAA TCAAACCCAC CCTTGTTTC GTCATATATC AAACCTGCTA GCAATTAAAT GGAATGTCAT GCCGTATTGA ATTCATTAAA ATTCATTAAA CCAATCACT CCGTATTGA ATTCATTAAA CCAATCACT CAAAGCAGCT CAAAGCAGCT	TAACATGCCC TCCTGTTTGC TCTGATGAGC CCCAGAGAGG GAGAGTGTCA CTGAGCAAAG CTGAGCTCGC CACCTGCTCC ACAGGGGACC TCCTTGGCTT CCTTGGCTT ATTTCTCTTA TCATCCTTCA AAGCCTTCTG CCTCCTCAG CTTTGATTCA TAAAGAGAAT AAACAAACAA GCCTTATTTA GTACTTTCCA ATGTTGCAAA TTCTAGATGA TTATTACAA	TTATCCGCAA TTCTTTCCTC AGTTGAAATC CCAAAGTACA CAGAGCAGGA CAGACTACGA TCAGTTCCAG TACCCCTATT TAATTATGCT CTCTCTTTCC TAAGGGACTA TCTATTTTA TCCTCACAGT CAAGCCCTCA ATTCCTGAG CATTCATTGC TAGGGAAATG CATTCTATTTAAA CAACCTAATT GGTTCTATAA CTGAGTGTCC AAGCCAAAAA	1740- 1800- 1860 1920 1980 2040 2100 2220 2280 2340 2400 2460 2520 2580 2640 2700 2760 2820 2880 2940 3000	
ACAACACACCACCAAGAACACACCACCAAACACACACAC	GGGATAAGCA CAAGGGCAGA GCTGCACCAT TCTGTTGTGT GATAACGCCC AGCACCTACA GTCTACGCCT AGGGGAGAGT TCCCATCCTT AGCTCATCTT GAGAATGAAT ATTATTATCT CATCCTAAGG CTCTGCAAGA ATGGTAGGAG TAAGGGTGAC AGCAAATTTT AAAATAACAA TCATGGTACT GGGACTCCTG TATACTGTGA CAAATATTT AAAAACTATG CCCGATTGTC	TGCTGTTTC ACTTTGTTAC CTGTCTTCAT GCCTGCTGAA TCCAATCGGG GCCTCAGCAG GTTAGAGGGA TGGCCTCTGA TCACCTCACC	ETGTCTGTCCC TTAAACACCA CTTCCCGCCA TAACTTCTAT TAACTCCAG CACCTGACG CATCAGGGC GAAGTGCCCC CCCTTTTTCC CCCCTCCTCC AATCTTTGCA CAACTACTCA TTATAAAAA TCAAACCCAC CCTTGTTTC GTCATATATC AAACCTGCTA GCAATTAAA GCAATCAT GCGTATTGA ATTCATTAAA CCAATCAT GCGTATTGA ATTCATTAAA CCAATCATTAAA CCAATCATTAAA CCAATCATTAAA CCAATCATTAAA CCAATCACCAC CAAAGCAGCT ATGAGTTATT	TAACATGCCC TCCTGTTTGC TCTGATGAGC CCCAGAGAGG GAGAGTGTCA CTGAGCAAAG CTGAGCTCGC CACCTGCTCC ACAGGGGACC TCCTTGGCTT CCTTGGCTT ATTTCTCTTA TCATCCTTCA AAGCCTTCTG CCTCCTCAG CTTTGATTCA TAAAGAGAAT AAACAAACAA GCCTTATTTA GTACTTTCCA ATGTTGCAAA TTCTAGATGA TTATTTACAA AAACTGTGGT	TTATCCGCAA TTCTTTCCTC AGTTGAAATC CCAAAGTACA CAGAGCAGGA CAGACTACGA TCAGTTCCAG TACCCCTATT TAATTATGCT CTCTCTTTCC TAAGGACTA TCTATTTTA TCCTCACAGT CAAGCCCTCA ATTCCTGAG CATTCATTGC TAGGGAAATG CATTCTTTAAA CAACCTAATT GGTTCTATAA CTGAGTGTCC AAGCCAAAAA ATGTTTATAC	1740- 1800- 1860 1920 1980 2040 2100 2160 2220 2280 2340 2400 2460 2520 2580 2640 2700 2760 2820 2880 2940 3000 3060	
ACAACACACCCAGGAACTGTG TGGAACTGCC GTGGAAGGAC GAACACAAA GAGCTTCAAC CCTGACCCCC GCGGTCCTCC AATGTTGGAG TCATTTAATA AATATGTAGT CCCTATCATC CCCCTGGCCC TAGTCCTTT AATCAACCAA AACATGATAT TTTAAGTTCA CAGGTACTGA TAATCCACAC AGCTGAGAGA CCACCCACCA TTGGAAATAC ATTAGAATAC	GGGATAAGCA CAAGGGCAGA GCTGCACCAT TCTGTTGTGT GATAACGCCC AGCACCTACA GTCTACGCCT AGGGGAGAGT TCCCATCCTT AGCTCATCTT GAGAATGAAT ATTATTATCT CATCCTAAGG CTCTGCAAGA ATGGTAGGAC TAAGGGTGAC AGCAAATTTT AAAATAACAA TCATGGTACT GGGACTCCTG TATACTGTGA CAAATATTT AAAAACTATG CCCGATTGTC CCAATGAGGA	TGCTGTTTCC TGTCTTCAT GCCTGCTGAA TCCAATCGGG GCCTCAGCAG GCGAAGTCAC GTTAGAGGGA TCACCTCACC	ETGTCTGTCGC TTAAACACCA TTAAACACCA TAACTTCTAT TAACTCCAG CACCTGACG CATCAGGGC GAAGTGCCCC CCCTTTTTCC CCCTCCTCC AATCTTTGCA TTATAAAAA TCAAACCCAC CCTTGTTTC GTCATATATC AAACCTACTA GCAATTAAAT GGAATGTCAT GCCGTATTGA ATTCATTAAA ATTCATTAAA GCAATCCCAC CAAAGCAGCT ATGAGTTATT GCTACAACTA	TAACATGCCC TCCTGTTTGC TCTGATGAGC CCCAGAGAGG GAGAGTGTCA CTGAGCAAAG CTGAGCTCGC CACCTGCTCC ACAGGGGACC TCCTTGGCTT ATTTCTCTTA TCATCCTTCA AAGCCTTCTG CCTCTCAG CTTTGATTCA TAAAGAGAAT AAACAAACAA GCCTTATTTA GTACTTCCA ATGTTGCAAA TTCTAGATGA TTATTACAA AAACTGTGGT TACCTACA	TTATCCGCAA TTCTTTCCTC AGTTGAAATC CCAAAGTACA CAGAGCAGGA CAGACTACGA TCAGTTCCAG TACCCCTATT TAATTATGCT CTCTCTTTCC TAAGGGACTA TCTATTTTA TCCTCACAGT CAAGCCCTCA ATTCCTGAG CATTCATTGC TAGGGAAATG CATTTTTAAA CAACCTAATT GGTTCTATAAA CTGAGTGTCC AAGCCAAAAA ATGTTTATAC CACAGATGAA	1740- 1800- 1860 1920 1980 2040 2100 2160 2220 2280 2340 2400 2460 2520 2580 2640 2700 2760 2820 2880 2940 3000 3060 3120	
ACAACACACCC AGGAACTGTG TGGAACTGCC GTGGAAGGTG GAGCAAGGAC GAAACACAAA GAGCTTCAAC CCTGACCCCC GCGGTCCTCC AATGTTGGAG TCATTTAATA AATATGTAGT CCCTATCATC CCCCTGGGCC TAGTCCTTT AATCAACCAA AACATGATAT TTTAAGTTCA CAGGTACTGA CAGCTACCAC AGCTGAGAGA CCACCCACCA TTGGAAATAC ATTAGAATAC TCTCATAAAA	GGGATAAGCA CAAGGGCAGA GCTGCACCAT TCTGTTGTGT GATAACGCCC AGCACCTACA GTCTACGCCT AGGGGAGAGT TCCCATCCTT AGCTCATCTT GAGAATGAAT ATTATTATCT CATCCTAAGG CTCTGCAAGA ATGGTAGGAC TAAGGGTGAC AGCAAATTTT AAAATAACAA TCATGGTACT GGGACTCCTG TATACTGTGA CAAATATTT AAAAACTATG CCCGATTGTC CCAATGAGGA ATATGTTAC	TGCTGTTTC ACTTTGTTAC CTGTCTTCAT GCCTGCTGAA TCCAATCGGG GCCTCAGCAG GTTAGAGGGA TGGCCTCTGA TCACCTCACC	ETGTCTGTCCC TTTAAACACCA CTTCCCGCCA TAACTTCTAT TAACTCCAG CACCTGACG CACCTGACG CATCAGGGC GAAGTGCCCC CCCTTTTTCC CCCTTCTCC AATCTTTGCA CAACTACTCA TTATAAAAA TCAAACCCAC CCTTGTTTC GTCATATATC AAACCTGCTA GCAATTAAAT GCAATTCAT GCAATTAAA ATTCATTAAA ATTCATTAAA CCAATCCAC CAAAGCAGCT ATGAGTTATT GCTACAACTA CTCAATGCAA CTCAATGCAA	TAACATGCCC TCCTGTTTGC TCTGATGAGC CCCAGAGAGG GAGAGTGTCA CTGAGCAAAG CTGAGCTCGC CACCTGCTCC ACAGGGGACC TCCTTGGCTT ATTTCTCTTA TCATCCTTCA AAGCCTTCTG CCTCTCAG CTTTGATTCA TAAAGAGAAT AAACAAACAA GCCTTATTTA GTACTTTCA ATGTTGCAAA TTCTAGATGA TTATTACAA AAACTGTGGT TACCTACTCA AAGCTTCTCA AAGCTTTCCA ATGTTGCAAA TTCTAGATGA TTATTTACAA AAACTGTGGT TACCTACTCA AAGATATGTT	TTATCCGCAA TTCTTTCCTC AGTTGAAATC CCAAAGTACA CAGAGCAGGA CAGACTACGA TCAGTTCCAG TACCCCTATT TAATTATGCT CTCTCTTTCC TAAGGGACTA TCTATTTTA TCCTCACAGT CAAGCCCTCA ATTCCTGAG CATTCATTGC TAGGGAAATG CATTCTTTAAA CAACCTAATT GGTTCTATAA CTGAGTGCC AAGCCAAAAA ATGTTTATAC CACAGATGAA CTGCAGATGAA CTGTATGTTT	1740- 1800- 1860 1920 1980 2040 2100 2160 2220 2340 2460 2520 2580 2640 2700 2760 2820 2880 2940 3000 3060 3120 3180	

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TCTTAGCTGG. GGGTGGGCGA GTTAGTGCCT GGGAGAAGAC AAGAAGGGGC TTCTGGGGTC
                                                                          3360
          TTGGTAATGT TCTGTTCCTC GTGTGGGGTT GTGCAGTTAT GATCTGTGCA CTGTTCTGTA
                                                                          3420
          TACACATTAT GCTTCAAAAT AACTTCACAT AAAGAACATC TTATACCCAG TTAATAGATA
          GAAGAGGAAT AAGTAATAGG TCAAGACCAA CGCAGCTGGT AAGTGGGGGC CTGGGATCAA
                                                                          3540
          ATAGCTACCT GCCTAATCCT GCCCWCTTGA GCCCTGAATG AGTCTGCCTT CCAGGGCTCA
                                                                          3600
          AGGTGCTCAA CAAAACAACA GGCCTGCTAT TTTCCTGGCA TCTGTGCCCT GTTTGGCTAG
          CTAGGAGCAC ACATACATAG AAATTAAATG AAACAGACCT TCAGCAAGGG GACAGAGGAC
                                                                          3720
                                                                          3780
          AGAATTAACC TTGCCCAGAC ACTGGAAACC CATGTATGAA CACTCACATG TTTGGGAAGG
          GGGAAGGCA CATGTAAATG AGGACTCTTC CTCATTCTAT GGGGCACTCT GGCCCTGCCC
                                                                          3840
          CTCTCAGCTA CTCATCCATC CAACACCT TTCTAAGTAC CTCTCTGC CTACACTCTG
                                                                          3900
          AAGGGGTTCA GGAGTAACTA ACACAGCATC CCTTCCCTCA AATGACTGAC AATCCCTTTG
                                                                          3960
          TCCTGCTTTG TTTTTCTTTC CAGTCAGTAC TGGGAAAGTG GGGAAGGACA GTCATGGAGA
                                                                          4020
                                                                          4080
          AACTACATAA GGAAGCACCT TGCCCTTCTG CCTCTTGAGA ATGTTGATGA GTATCAAATC
          TTTCAAACTT TGGAGGTTTG AGTAGGGGTG AGACTCAGTA ATGTCCCTTC CAATGACATG
                                                                          4140
          AACTTGCTCA CTCATCCCTG GGGGCCAAAT TGAACAATCA AAGGCAGGCA TAATCCAGTT
                                                                          4200
          ATGAATTCTT GCGGCCGCTT GCTAGCTTCA CGTGTTGGAT CCAACCGCGG AAGGGCCCTA
          TTCTATAGTG TCACCTAAAT GCTAGAGCTC GCTGATCAGC CTCGACTGTG CCTTCTAGTT
                                                                          4320
          GCCAGCCATC TGTTGTTTGC CCCTCCCCG TGCCTTCCTT GACCCTGGAA GGTGCCACTC
                                                                          4380
          CCACTGTCCT TTCCTAATAA AATGAGGAAA TTGCATCGCA TTGTCTGAGT AGGTGTCATT
                                                                          4440
          CTATTCTGGG GGGTGGGGTG GGGCAGGACA GCAAGGGGGA GGATTGGGAA GACAATAGCA
                                                                          4500
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                                                                          4560
          CTAGGGGGTA TCCCCACGCG CCCTGTAGCG GCGCATTAAG CGCGGCGGGT GTGGTGGTTA
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          CTTCCTTTCT CGCCACGTTC GCCGGGCCTC TCAAAAAAGG GAAAAAAAGC ATGCATCTCA
                                                                          4740
          ATTAGTCAGC AACCATAGTC CCGCCCCTAA CTCCGCCCAT CCCGCCCCTA ACTCCGCCCA
                                                                          4800
          GTTCCGCCCA TTCTCCGCCC CATGGCTGAC TAATTTTTTT TATTTATGCA GAGGCCGAGG
                                                                          4860
CCGCCTCGGC CTCTGAGCTA TTCCAGAAGT AGTGAGGAGG CTTTTTTGGA GGCCTAGGCT 4920
THAT AND TITTGCAAAAA GCTTGGACAG CTCAGGGCTG CGATTTCGCG CCAAACTTGA CGGCAATCCT 4980 TO THE ACADAMETER STATES
AGCGTGAAGG-CTGGTAGGAT TTTATCCCCG CTGCCATGAT GGTTCGACCA TTGAACTGCA 1 5040
TCGTCGCCGT GTCCCAAAAT ATGGGGATTG GCAAGAACGG AGACCTACCC TGGCCTCCGC 5100 THE FORM
AGAATCTGGT GATTATGGGT AGGAAAACCT GGTTCTCCAT TCCTGAGAAG AATCGACCTT 5220
   INTERNATIONAL STANAGGACAG AATTAATATA GTTCTCAGTA GAGAACTCAA AGAACCACCA CGAGGAGCTC 5280 STANAGA FUR AND AND A SE
 ATTTTCTTGC CAAAAGTTTG GATGATGCCT TAAGACTTAT TGAACAACCG GAATTGGCAA 5340 ; 5340 ; 5340
                                                                          GTAAAGTAGA CATGGTTTGG ATAGTCGGAG GCAGTTCTGT TTACCAGGAA GCCATGAATC
          AACCAGGCCA CCTTAGACTC TTTGTGACAA GGATCATGCA GGAATTTGAA AGTGACACGT
                                                                          5460
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                                                                          6000
          6060
          AGCTGCACTG CTATACAAGA AAATTATGGA AAAATATTCT GTAACCTTTA TAAGTAGGCA
                                                                          6120
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                                                                          6480
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                                                                          6540
          ATCTCATGCT GGAGTTCTTC GCCCACCCCA ACTTGTTTAT TGCAGCTTAT AATGGTTACA
                                                                          6600
          AATAAAGCAA TAGCATCACA AATTTCACAA ATAAAGCATT TTTTTCACTG CATTCTAGTT
                                                                          6660
          GTGGTTTGTC CAAACTCATC AATGTATCTT ATCATGTCTG TATACCGTCG ACCTCTAGCT
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AGAGCTTGGC	GTAATCATGG	TCATAGCTGT	TTCCTGTGTG	AAATTGTTAT	CCGCTCACAA	6780			
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GCTAACTCAC	ATTAATTGCG	TTGCGCTCAC	TGCCCGCTTT	CCAGTCGGGA	AACCTGTCGT	6900			+
GCCAGCTGCA	TTAATGAATC	GGCCAACGCG	CGGGGAGAGG	CGGTTTGCGT	ATTGGGCGCT	6960			
CTTCCGCTTC	CTCGCTCACT	GACTCGCTGC	GCTCGGTCGT	TCGGCTGCGG	CGAGCGGTAT	7020			
CAGCTCACTC	AAAGGCGGTA	ATACGGTTAT	CCACAGAATC	AGGGGATAAC	GCAGGAAAGA	7080			
		CAAAAGGCCA							
		CCTGACGAGC							
		TAAAGATACC							
		CCGCTTACCG							
		TCACGCTGTA							
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		CCGGTAAGAC							
		AGGTATGTAG							
		AGGACAGTAT							
CCTTCGGAAA	AAGAGTTGGT	AGCTCTTGAT	CCGGCAAACA	AACCACCGCT	GGTAGCGGTG	7680			
		CAGATTACGC							
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TCATGAGATT	ATCAAAAAGG	ATCTTCACCT	AGATCCTTTT	AAATTAAAA	TGAAGTTTTA				
AATCAATCTA	AAGTATATAT	GAGTAAACTT	GGTCTGACAG	TTACCAATGC	TTAATCAGTG				
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TGTAGATAAC	TACGATACGG	GAGGGCTTAC	CATCTGGCCC	CAGTGCTGCA	ATGATACCGC	8040			
GAGACCCACG	CTCACCGGCT	CCAGATTTAT	CAGCAATAAA	CCAGCCAGCC	GGAAGGGCCG				
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***********		CCAGTTAATA							
		TCGTTTGGTA							
CAAGGCGAGT									
CGATCGTTGT									
ATAATTCTCT							والمراكبين السيواءات		
CCAAGTCATT							* * *2		٠ :
		AGCAGAACTT					งส์	-	· .
CGGGGCGAAA	'ACTCTCAAGG	ATCTTACCGC	TGTTGAGATC	CAGITCGATG	TAACCCACTC	8640			
2	+ - +	${\tt GCATCTTTTA}$	_	-			1		
CAGGAAGGCA	AAATGCCGCA	AAAAAGGGAA	TAAGGGCGAC	ACGGAAATGT	TGAATACTCA		10 gr#54		-
TACTCTTCCT	TTTTCAATAT	TATTGAAGCA	TTTATCAGGG	TTATTGTCTC	ATGAGCGGAT	8820-	0.03	-	
ACATATTTGA	ATGTATTTAG	AAAAATAAAC	AAATAGGGGT	TCCGCGCACA	TTTCCCCGAA	8880			
AAGTGCCACC	TGACGTC					8897			

44

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAAGAGGAAG ACTGACGGTG CCCCCGCGAG TTCAGGTGCT GAGG

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: Single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
CCTCAGCACC TGAACTCGCG GGGGCACCGT CAGTCTTCCT CTTC	44
(2) INFORMATION FOR SEQ ID NO:16:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 51 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:	
CTGGGAGGGC TTTGTTGGAG ACCGAGCACG AGTACGACTT GCCATTCAGC C	51
(2) INFORMATION FOR SEQ ID NO:17:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	w 1.6 m
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
GATGGTTTTC TCGATGGCGG CTGGGAGGGC	30
(2) INFORMATION FOR SEQ ID NO:18:	,
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 30 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
GCCCTCCCAG CCGCCATCGA GAAAACCATC	30
(2) INFORMATION FOR SEQ ID NO:19:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 34 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
GATGGTTTTC TCGATAGCGG CTGGGAGGGC TTTG
(2) INFORMATION FOR SEQ ID NO:20:
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 81 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
GATGGTTTTC TCGATGGCGG CTGGGAGGGC TTTGTTGGAG ACCGAGCACG AGTACGACTT GCCATTCAGC CAGTCCTGGT G 81
(2) INFORMATION FOR SEQ ID NO:21:
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 81 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS:—single (D) TOPOLOGY: linear (LL) MOLECULE TYPE: CDNA
(LL) MOLECULE TYPE: CDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
CACCAGGACT GGCTGAATGG CAAGTCGTAC TCGTGCTCGG TCTCCAACAA AGCCCTCCCA GCCGCCATCG AGAAAACCAT C
(2) INFORMATION FOR SEQ ID NO:22:
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 8690 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22: GGTACCAATT TAAATTGATA TCTCCTTAGG TCTCGAGTCT CTAGATAACC GGTCAATCGA TTGGAATTCT TGCGGCCGCT TGCTAGCCAC CATGGAGTTG TGGTTAAGCT TGGTCTTCCT TGTCCTTGTT TTAAAAGGTG TCCAGTGTA AGTGCAACTG GTGGAGTCTG GGGGAGGCTT AGTGCAGCCT GGAGGGTCCC TGCGACTTTC CTGTGCTGCA TCTGGATTCC CGTTCAGTGA CTATTACATG TATTGGGTTC GCCAGGCTCC AGGCAAGGGA CTGGAGTGGG TCTCATACAT TAGTCAAGAT GGTGATATAA CCGACTATGC AGACTCCGTA AAGGGTCGAT TCACCATCTC CAGAGACAAT GCCAAAGAACA GCCTGTACCT GCAAATGAAC AGCCTGAGGG ACGAGGACAC 420
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was the Gregoritest caaactcate aatgtatett ateatgtets, tataeege acctetaget to 5520 and a significant
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(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 7874 base pairs

 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear.
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

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                                                                      4140
  TCCACACAGG CATAGAGTGT CTGCTATTAA TAACTATGCT CAAAAATTGT GTACCTTTAG
                                                                      4200
  CTTTTTAATT TGTAAAGGGG TTAATAAGGA ATATTTGATG TATAGTGCCT TGACTAGAGA
                                                                      4260 ·
  TCATAATCAG CCATACCACA TTTGTAGAGG TTTTACTTGC TTTAAAAAAC CTCCCACACC
                                                                      4320
  TCCCCCTGAA CCTGAAACAT AAAATGAATG CAATTGTTGT TGTTAACTTG TTTATTGCAG
                                                                      4380
  CTTATAATGG TTACAAATAA AGCAATAGCA TCACAAATTT CACAAATAAA GCATTTTTTT
                                                                      4440
  CACTGCATTC TAGTTGTGGT TTGTCCAAAC TCATCAATGT ATCTTATCAT GTCTGGATCG
                                                                      4500
  GCTGGATGAT CCTCCAGCGC GGGGATCTCA TGCTGGAGTT CTTCGCCCAC CCCAACTTGT
                                                                      4560
TTATTGCAGC TTATAATGGT TACAAATAAA GCAATAGCAT CACAAATTTC ACAAATAAAG
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CATTTTTTC ACTGCATTCT AGTTGTGGTT TGTCCAAACT CATCAATGTA TCTTATCATG
                                                                                                                4680
           TCTGTATACC GTCGACCTCT AGCTAGAGCT TGGCGTAATC ATGGTCATAG CTGTTTCCTG
           TGTGAAATTG TTATCCGCTC ACAATTCCAC ACAACATACG AGCCGGAAGC ATAAAGTGTA
           AAGCCTGGGG TGCCTAATGA GTGAGCTAAC TCACATTAAT TGCGTTGCGC TCACTGCCCG
                                                                                                                4860
           CTTTCCAGTC GGGAAACCTG TCGTGCCAGC TGCATTAATG AATCGGCCAA CGCGCGGGGA
                                                                                                                4920
           GAGGCGGTTT GCGTATTGGG CGCTCTTCCG CTTCCTCGCT CACTGACTCG CTGCGCTCGG
                                                                                                                4980
           TCGTTCGGCT GCGGCGAGCG GTATCAGCTC ACTCAAAGGC GGTAATACGG TTATCCACAG
                                                                                                                5040
           AATCAGGGGA TAACGCAGGA AAGAACATGT GAGCAAAAAG CCCAGCAAAAG GCCAGGAACC
                                                                                                               5100
           GTAAAAAGGC CGCGTTGCTG GCGTTTTTCC ATAGGCTCCG CCCCCTGAC GAGCATCACA
           AAAATCGACG CTCAAGTCAG AGGTGGCGAA ACCCGACAGG ACTATAAAGA TACCAGGCGT
                                                                                                                5220
           TTCCCCCTGG AAGCTCCCTC GTGCGCTCTC CTGTTCCGAC CCTGCCGCTT ACCGGATACC
                                                                                                                5280
           TGTCCGCCTT TCTCCCTTCG GGAAGCGTGG CGCTTTCTCA ATGCTCACGC TGTAGGTATC
                                                                                                                5340
           TCAGTTCGGT GTAGGTCGTT CGCTCCAAGC TGGGCTGTGT GCACGAACCC CCCGTTCAGC
                                                                                                               5400
           CCGACCGCTG CGCCTTATCC GGTAACTATC GTCTTGAGTC CAACCCGGTA AGACACGACT
                                                                                                               5460
           TATCGCCACT GGCAGCAGCC ACTGGTAACA GGATTAGCAG AGCGAGGTAT GTAGGCGGTG
                                                                                                               5520
           CTACAGAGTT CTTGAAGTGG TGGCCTAACT ACGGCTACAC TAGAAGGACA GTATTTGGTA
           TCTGCGCTCT GCTGAAGCCA GTTACCTTCG GAAAAAGAGT TGGTAGCTCT TGATCCGGCA
                                                                                                                5640
           AACAAACCAC CGCTGGTAGC GGTGGTTTTT TTGTTTGCAA GCAGCAGATT ACGCGCAGAA
                                                                                                                5700
                                                                                                                5760
           AAAAAGGATC TCAAGAAGAT CCTTTGATCT TTTCTACGGG GTCTGACGCT CAGTGGAACG
           AAAACTCACG TTAAGGGATT TTGGTCATGA GATTATCAAA AAGGATCTTC ACCTAGATCC
                                                                                                                5820
           TTTTAAATTA AAAATGAAGT TTTAAATCAA TCTAAAGTAT ATATGAGTAA ACTTGGTCTG
                                                                                                                5880
           ACAGTTACCA ATGCTTAATC AGTGAGGCAC CTATCTCAGC GATCTGTCTA TTTCGTTCAT
                                                                                                               5940
           CCATAGTTGC CTGACTCCCC GTCGTGTAGA TAACTACGAT ACGGGAGGGC TTACCATCTG
                                                                                                                6000
           GCCCCAGTGC TGCAATGATA CCGCGAGACC CACGCTCACC GGCTCCAGAT TTATCAGCAA
                                                                                                                6060
           TAAACCAGCC AGCCGGAAGG GCCGAGCGCA GAAGTGGTCC TGCAACTTTA TCCGCCTCCA
                                                                                                                6120
           TCCAGTCTAT TAATTGTTGC CGGGAAGCTA GAGTAAGTAG TTCGCCAGTT AATAGTTTGC
                                                                                                               6180
     GCAACGTTGT TGCCATTGCT ACAGGCATCG TGGTGTCACG CTCGTCGTTT GGTATGGCTT. . 6240.
ALE AND - CATTCAGCTC CGGTTCCCAA CGATCAAGGC GAGTTACATG ATCCCCCATG TTGTGCAAAA AA6300 - A A ATGENT OF A ATCCCCCATG TTGTGCAAAA AA6300 - A A ATGENT OF A ATCCCCCATG TTGTGCAAAA AA6300 - A A ATGENT OF A ATCCCCCATG TTGTGCAAAA AA6300 - A A ATGENT OF A ATCCCCCATG TTGTGCAAAA AA6300 - A A ATGENT OF A ATCCCCCATG TTGTGCAAAA AA6300 - A A ATGENT OF A ATCCCCCATG TTGTGCAAAA AA6300 - A A ATGENT OF ATGENT OF A ATCCCCCATG TTGTGCAAAA AA6300 - A ATGENT OF A ATCCCCCATG TTGTGCAAAA AA6300 - A ATGENT OF A ATCCCCCCATG TTGTGCAAAA AA6300 - A ATGENT OF ATGENT OF ATCCCCCATG TTGTGCAAAA AA6300 - A ATGENT OF ATGENT OF ATCCCCCATG TTGTGCAAAA AA6300 - A ATGENT OF ATG
AAGCGGTTAG CTCCTTCGGT CCTCCGATCG TTGTCAGAAG TAAGTTGGGC GCAGTGTTAT 6360
          CACTCATGGT TATGGCAGCA CTGCATAATT CTCTTACTGT CATGCCATCC GTAAGATGCT
                                                                                                               6420
 TTTCTGTGACTGGTGAGTAC TCAACCAAGT CATTCTGAGA.ATAGTGTATG CGGCGACCGATT6480 311 107 11 1111
       GTTGCTCTTG CCCGGCGTCA ATACGGGATA ATACCGCGCC ACATAGCAGA ACTTTAAAAG ....6540
                                                                                                               6600
 TGCTCATCAT TGGAAAACGT TCTTCGGGGC GAAAACTCTC AAGGATCTTA CCGCTGTTGA
                                                                                                               6660
THE GATCCAGTTC GATGTAACCC ACTCGTGCAC CCAACTGATC TTCAGCATCT TTTACTTTCA
                                                                                                                6720 ... - ...
    CCAGCGTTTC TGGGTGAGCA AAAACAGGAA GGCAAAATGC CGCAAAAAAG GGAATAAGGG
           CGACACGGAA ATGTTGAATA CTCATACTCT TCCTTTTTCA ATATTATTGA AGCATTTATC
           AGGGTTATTG TCTCATGAGC GGATACATAT TTGAATGTAT TTAGAAAAAT AAACAAATAG
                                                                                                                6840
           GGGTTCCGCG CACATTTCCC CGAAAAGTGC CACCTGACGT CGACGGATCG GGAGATCTGC
                                                                                                                6900
           TAGGTGACCT GAGGCGCGC GGCTTCGAAT AGCCAGAGTA ACCTTTTTTT TTAATTTTAT
                                                                                                                6960
           TTTATTTTAT TTTTGAGATG GAGTTTGGCG CCGATCTCCC GATCCCCTAT GGTCGACTCT
                                                                                                                7020
           CAGTACAATC TGCTCTGATG CCGCATAGTT AAGCCAGTAT CTGCTCCCTG CTTGTGTGTT
                                                                                                               7080
           GGAGGTCGCT GAGTAGTGCG CGAGCAAAAT TTAAGCTACA ACAAGGCAAG GCTTGACCGA
                                                                                                               7140
           CAATTGCATG AAGAATCTGC TTAGGGTTAG GCGTTTTGCG CTGCTTCGCG ATGTACGGGC
           CAGATATACG CGTTGACATT GATTATTGAC TAGTTATTAA TAGTAATCAA TTACGGGGTC
                                                                                                                7260
           ATTAGTTCAT AGCCCATATA TGGAGTTCCG CGTTACATAA CTTACGGTAA ATGGCCCGCC
                                                                                                                7320
           TGGCTGACCG CCCAACGACC CCCGCCCATT GACGTCAATA ATGACGTATG TTCCCATAGT
                                                                                                                7380
           AACGCCAATA GGGACTTTCC ATTGACGTCA ATGGGTGGAC TATTTACGGT AAACTGCCCA
                                                                                                                7440
           CTTGGCAGTA CATCAAGTGT ATCATATGCC AAGTACGCCC CCTATTGACG TCAATGACGG
                                                                                                               7500
           TAAATGGCCC GCCTGGCATT ATGCCCAGTA CATGACCTTA TGGGACTTTC CTACTTGGCA
                                                                                                               7560
           GTACATCTAC GTATTAGTCA TCGCTATTAC CATGGTGATG CGGTTTTGGC AGTACATCAA
                                                                                                               7620
           TGGGCGTGGA TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA
                                                                                                               7680
           TGGGAGTTTG TTTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA ACAACTCCGC
                                                                                                                7740
                                                                                                                7800
           CCCATTGACG CAAATGGGCG GTAGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTCT
           CTGGCTAACT AGAGAACCCA CTGCTTACTG GCTTATCGAA ATTAATACGA CTCACTATAG
                                                                                                               7860
                                                                                                               7874
           GGAGACCCAA GCTT
```

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly 10 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ser Asp Tyr 25 Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 40 Ser Tyr Ile Ser Gln Asp Gly Asp Ile Thr Asp Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr 70 75 Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys 90 Ala Arg Gly Leu Ala Asp Gly Ala Trp Phe Ala Tyr Trp Gly Gln Gly 100 105 Thr Leu Val Thr Val Ser Ser 115

(2) INFORMATION FOR SEQ ID NO: 25 the analysis and the second of the sec

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 amino acids
 - (B) TYPE: amino acid

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys 10 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr 25 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser 55 60 Leu Ser Ser Val Val Thr Val Pro Ser Ser Leu Gly Thr Gln Thr 70 75 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys 90 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys 105 110 100 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro 120 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys 135

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Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp 155 150 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu 170 175 165 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu 190 185 180 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Asp Lys Val Ser Asn 200 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly 220 215 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu 235 230 Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr 250 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn 265 260 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe 280 285 275 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn 300 295 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr 310 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys 325

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
- - (B) TYPE: amino acid
 - STRANDEDNESS single and the

- (D) TOPOLOGY: linear ...
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ala 1	Ser	Thr	Lys	Gly 5	Pro	Ser	Val	Phe	Pro 10	Leu	Ala	Pro	Ser	Ser 15	Lys
Ser	Thr	Ser	Gly 20	Gly	Thr	Ala	Ala	Leu 25	Gly	Cys	Leu	Val	Lys 30	Asp	Tyr
Phe	Pro	Glu 35	Pro	Val	Thr	Val	Ser 40	Trp	Asn	Ser	Gly	Ala 45	Leu	Thr	Ser
Gly	Val 50	His	Thr	Phe	Pro	Ala 55	Val	Leu	Gln	Ser	Ser 60	Gly	Leu	Tyr	Ser
Leu 65	Ser	Ser	Val	Val	Thr 70	Val	Pro	Ser	Ser	Ser 75	Leu	Gly	Thr	Gln	Thr 80
Tyr	Ile	Cys	Asn	Val 85	Asn	His	Lys	Pro	Ser 90	Asn	Thr	Lys	Val	Asp 95	Lys
Lys	Val		Pro 100	Lys	Ser	Cys	Asp	Lys 105	Thr	His	Thr	Cys	Pro 110	Pro	Сув
Pro	Gly	Gln 115	Pro	Arg	Glu	Pro	Gln 120	Val	Tyr	Thr	Leu	Pro 125	Pro	Ser	Arg
Asp	Glu 130	Leu	Thr	Lys	Asn	Gln 135	Val	Ser	Leu	Thr	Cys 140	Leu	Val	Lys	Gly
Phe 145	Tyr	Pro	Ser	Asp	Ile 150	Ala	Val	Glu	Trp	Glu 155	Ser	Asn	Gly	Gln	Pro 160

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Glu 1	Val	Asn	Leu	Val	Glu	Ser	Gly	Gly	Gly 10	Leu	Val	Gln	Pro	Gly 15	Gly
Ser	Leu	Lys	Val 20	Ser	Суѕ	Val	Thr	Ser 25	Gly	Phe	Thr	Phe	Ser 30	Asp	Tyr
Tyr	Met	Tyr 35	Trp	Val		Gln	Thr 40	Pro	Glu	Lys	Arg	Leu 45	Glu	Trp	Val
	Tyr.				-	_	_	Ile		Asp	Tyr 60		_	Thr	
	Gly.								Asn		Lys	Asn	Thr	Leu	Tyr 80 ~
	Gln		ser	Arg		Lys	Ser		Asp 90	Thr	`Ala`	Met	-	Tyr 95	Cys
Ala	Arg	Gly:	Leu 100	Asp	Asp	Gly	Ala	Trp 105	Phe	Ala	Tyr	Trp	Gly 110	Gln	Gly
Thr	Leu	Val 115	Thr	Val	Ser	Val	Ala 120	Ser	Thr	Lys	Gly	Pro 125	Ser	Val	Phe
Pro	Leu 130	Ala	Pro	Ser	Ser	Lys 135	Ser	Thr	Ser	Gly	Gly 140	Thr	Ala	Ala	Leu
Gly 145	Cys	Leu	Val	Lys	Asp 150	Tyr	Phe	Pro	Glu	Pro 155	Val	Thr	Val	Ser	Trp 160
Asn	Ser	Gly	Ala	Leu 165	Thr	Ser	Gly	Val	His 170	Thr	Phe	Pro	Ala	Val 175	Leu
Gln	Ser	Ser	Gly 180	Leu	Tyr	Ser	Leu	Ser 185	Ser	Val	Val	Thr	Val 190	Pro	Ser
Ser	Ser	Leu 195	Gly	Thr	Gln	Thr	Tyr 200	Ile	Cys	Asn	Val	Asn 205	His	Lys	Pro
Ser	Asn 210	Thr	Lys	Val	Asp	Lys 215	Lys	Val	Glu	Pro	Lys 220	Ser	Cys	Asp	Lys
Thr 225	His	Thr	Cys	Pro	Pro 230	Cys	Pro	Gly	Gln	Pro 235	Arg	Glu ·	Pro	Gln	Val 240
Tyr	Thr	Leu	Pro	Pro 245	Ser	Arg	Asp	Glu	Leu 250	Thr	Lys	Asn	Gln	Val 255	Ser
Leu	Thr	Cys	Leu 260	Val	Lys	Ġly	Phe	Tyr 265	Pro	Ser	Asp	Ile	Ala 270	Val	Glu
Trp	Glu	Ser 275	Asn	Gly	Gln	Pro	Glu 280	Asn	Asn	Tyr	Lys	Thr 285	Thr	Pro	Pro

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Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                        295
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
                    310
                                        315
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
                                    330
Pro Gly Lys
```

- (2) INFORMATION FOR SEQ ID NO:28:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8897 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CTGCCTAGCC	CTCTAGACGA	TCCACTGGAC	TCCGCGCGGC	CGAAGCTTAT	CGGTCTCATT	60		•
GGAAAAAAAA	ATTAAAATAA	AATAAAATAA	AAACTCTACC	TCAAACCGCG	GCTAGAGGGC	120		
TAGGGGATAC	CAGCTGAGAG	TCATGTTAGA	CGAGACTACG	GCGTATCAAT	TCGGTCATAG	180		
ACGAGGGACG	AACACACAAC	CTCCAGCGAC	TCATCACGCG	${\tt CTCGTTTTAA}$	ATTCGATGTT	240		
GTTCCGTTCC	GAACTGGCTG	TTAACGTACT	TCTTAGACGA	ATCCCAATCC	GCAAAACGCG	300		
ACGAAGCGCT	ACATGCCCGG	TCTATATGCG	CAACTGTAAC	TAATAACTGA	TCAATAATTA	360		
TCATTAGTTA	ATGCCCCAGT	AATCAAGTAT	CGGGTATATA	CCTCAAGGCG	CAATGTATTG	420		
AATGCCATTT	ACCGGGCGGA	CCGACTGGCG	GGTTGCTGGG	GGCGGGTAAC	TGCAGTTATT.	480	a control of the	The Direction
		TGCGGTTATC						
		AACCGTCATG						
-GATAACTGCA								
CCCTGAAAGG	TATGAACCGTC	ATGTAGATGC	ATAATCAGTA"	GCGATAATGG	TACCACTACG	720	*	
		CCCGCACCTA						
		CCCTCAAACA						
		GGTAACTGCG						
		ACCGATTGAT						
AATTATGCTG	AGTGATATCC	CTCTGGGTTC	GAACCATGGT	TAAATTTAAC	TATAGAGGAA	1020	•	
TCCAGAGCTC	${\tt AGAGATCTAT}$	TGGCCAGTTA	GCTAACCTTA	AGAACGCCGG	CGAACGATCG	1080		(8)
GTGGTACCTC	AACACCAATT	CGAACCAGGA	AGGAACAGGA	ACAAAATTTT	CCACAGGTCA	1140		
CACTTCACTT	AGACCACCTC	AGACCCCCTC	CGAATCACGT	CGGACCTCCC	AGGGACTTTC	1200		
AGAGGACACA	TTGGAGACCT	AAGTGAAAGT	CACTGATAAT	GTACATAACC	CAAGCGGTCT	1260		
GAGGTCTCTT	CTCCGACCTC	ACCCAGCGTA	TGTAATÇAGT	TCCACCACTA	TATTGGCTGA			
TAGGTCTGTG	ACATTTCCCA	GCTAAGTGGT	AGAGGTCTCT	GTTACGGTTC	TTGTGGGACA	1380		
		TTCAGACTCC						
ACCTGCTGCC	CCGGACCAAA	CGAATGACCC	CGGTTCCCTG	AGACCAGTGC	CAGAGACATC			
GATCGTGGTT	CCCGGGTAGC	CAGAAGGGGG	ACCGTGGGAG	GAGGTTCTCG	TGGAGACCCC	1560		**
CGTGTCGCCG	GGACCCGACG	GACCAGTTCC	TGATGAAGGG	GCTTGGCCAC	TGCCACAGCA	1620		
		TCGCCGCACG				1680		
		CACCAGTGGC				1740		
TGTAGACGTT	GCACTTAGTG	TTCGGGTCGT	TGTGGTTCCA	CCTGTTCTTT	CAACCACTCT	1800		
CCGGTCGTGT	CCCTCCCTCC	CACAGACGAC	CTTCGGTCCG	AGTCGCGAGG	ACGGACCTGC	1860		
		TCAGGTCCCG				1920		
GCCTCCGGAG	ACGGGCGGG	TGAGTACGAG	TCCCTCTCCC	AGAAGACCGA	AAAAGGGGTC	1980		
		TCCACGGGGA						
		CTCGGTATAG						
		TGAGGGAGTC						
CATTGAGGGT	TAGAAGAGAG	ACGTCTCGGG	TTTAGAACAC	TGTTTTGAGT	GTGTACGGGT	2220		•

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GGCACGGGTC CATTCGGTCG GGTCCGGAGC GGGAGGTCGA GTTCCGCCCT GTCCACGGGA
                                                                       2280
     TCTCATCGGA CGTAGGTCCC TGTGTGGTGC ACCCATGGTT GTACAGGCCT CGGTGTACCT
     GTCTCCGGCC GAGCCGGGTG GGAGACGGGA CTCTCACTGG CGACATGGTT GGAGACAGGG
     ATGTCCCGTC GGGGCTCTTG GTGTCCACAT GTGGGACGGG GGTAGGGCCC TACTCGACTG
                                                                       2460
     GTTCTTGGTC CAGTCGGACT GGACGGACCA GTTTCCGAAG ATAGGGTCGC TGTAGCGGCA
                                                                       2520
     CCTCACCCTC TCGTTACCCG TCGGCCTCTT GTTGATGTTC TGGTGCGGAG GGCACGACCT
                                                                       2580
     GAGGCTGCCG AGGAAGAAGG AGATGTCGTT CGAGTGGCAC CTGTTCTCGT CCACCGTCGT
                                                                       2640
     CCCCTTGCAG AAGAGTACGA GGCACTACGT ACTCCGAGAC GTGTTGGTGA TGTGCGTCTT
                                                                       2700
     CTCGGAGAGG GACAGAGGCC CATTTACTCA CGCTGCCGGC CGTTCGGGGG CGAGGGGCCC
     GAGAGCGCCA GCGTGCTCCT ACGAACCGTG CATGGGGGGAC ATGTATGAAG GGCCCGCGGG
     TCGTACCTTT ATTTCGTGGG TCGCGACGGG ACCCGGGGAC GCTCTGACAC TACCAAGAAA
                                                                       2880
     GGTGCCCAGT CCGGCTCAGA CTCCGGACTC ACCGTACTCC CTCCGTCTCG CCCAGGGTGA
                                                                       2940
     CAGGGGTGTG ACCGGGTCCG ACACGTCCAC ACGGACCCGG GGGATCCCAC CCCGAGTCGG
                                                                       3000
     TCCCCGACGG GAGCCGTCCC ACCCCTAAA CGGTCGCACC GGGAGGGAGG TCGTCGTGGA
                                                                       3060
     CGGGACCCGA CCCGGTGCCC TTCGGGATCC TCGGGGACCC CTGTCTGTGT GTCGGGGACG
                                                                       3120
     GAGACATCCT CTGACAGGAC AAGACACTCG CGGGGACAGG AGGGCTGGAG GTACGGGTGA
     GCCCCGTAC GGATCAGGTA CACGCATCCC TGTCCGGGAG GGAGTGGGTA GATGGGGGTG
                                                                       3240
     CCGTGATTGG GGACCGACGG GACGGGTCGG AGCGTGGGCG TACCCCTGTG TTGGCTGAGG
                                                                       3300
     CCCCTGTACG TGAGAGCCCG GGACACCTCC CTGACCACGT CTACGGGTGT GTGTGTGAGT
                                                                       3360
     CGGGTCTGGG CAAGTTGTTT GGGGCGTGAC TCCAACCGGC CGGTGTGCCG GTGGTGTGTG
                                                                       3420
     TGTGCACGTG CGGAGTGTGT GCCTCGGAGT GGGCCCGCTT GACGTGTCGT GGGTCTGGTC
                                                                       3480
     TCGTTCCAGG AGCGTGTGCA CTTGTGAGGA GCCTGTGTCC GGGGGTGCTC GGGGTGCGCC
                                                                       3540
     GTGGAGTTCC GGGTGCTCGG AGAGCCGTCG AAGAGGTGTA CGACTGGACG AGTCTGTTTG
                                                                       3600
     GGTCGGGAGG AGAGTGTTCC CACGGGGACG TCGGCGGTGT GTGTGTGTCC CCTAGTGTGT
                                                                       3660
     GGTGCAGTGC AGGGACCGGG ACCGGGTGAA GGGTCACGGC GGGAAGGGAC GTCCTGCCTA
                                                                       3720
     GTCGGAGCTG ACACGGAAGA TCAACGGTCG GTAGACAACA AACGGGGAGG GGGCACGGAA
                                                                       3780
     GGAACTGGGA CCTTCCACGG TGAGGGTGAC AGGAAAGGAT TATTTTACTC CTTTAACGTA
                                                                     3840
3900 -- ...
CCCTCCTAAC CCTTCTGTTA TCGTCCGTAC GACCCCTACG CCACCCGAGA TACCGAAGAC 3960 3960
   - TCCGCCTTTC TTGGTCGACC CCGAGATCCC CCATAGGGGT GCGCGGGACA TCGCCGCGTA
                                                                      4020
     GCGGGCGAGG AAAGCGAAAG AAGGGAAGGA AAGAGCGGTG CAAGCGGCCC GGAGAGTTTT 4140 ---
    TTCCCTTTTT TTCGTACGTA GAGTTAATCA GTCGTTGGTA TCAGGGCGGG GATTGAGGCG
                                                                      4200 ....
                                                                     4260
    GGTAGGGCGG GGATTGAGGC GGGTCAAGGC GGGTAAGAGG CGGGGTACCG ACTGATTAAA
     AAAAATAAAT ACGTCTCCGG CTCCGGCGGA GCCGGAGACT CGATAAGGTC TTCATCACTC
                                                                      4320
     CTCCGAAAAA ACCTCCGGAT CCGAAAACGT TTTTCGAACC TGTCGAGTCC CGACGCTAAA
     GCGCGGTTTG AACTGCCGTT AGGATCGCAC TTCCGACCAT CCTAAAATAG GGGCGACGGT
                                                                      4440
     AGTACCAAGC TGGTAACTTG ACGTAGCAGC GGCACAGGGT TTTATACCCC TAACCGTTCT
                                                                       4500
     TGCCTCTGGA TGGGACCGGA GGCGAGTCCT TGCTCAAGTT CATGAAGGTT TCTTACTGGT
                                                                       4560
     GTTGGAGAAG TCACCTTCCA TTTGTCTTAG ACCACTAATA CCCATCCTTT TGGACCAAGA
                                                                      4620
     GGTAAGGACT CTTCTTAGCT GGAAATTTCC TGTCTTAATT ATATCAAGAG TCATCTCTTG
                                                                      4680
     AGTTTCTTGG TGGTGCTCCT CGAGTAAAAG AACGGTTTTC AAACCTACTA CGGAATTCTG
     AATAACTTGT TGGCCTTAAC CGTTCATTTC ATCTGTACCA AACCTATCAG CCTCCGTCAA
     GACAAATGGT CCTTCGGTAC TTAGTTGGTC CGGTGGAATC TGAGAAACAC TGTTCCTAGT
                                                                      4860
     ACGTCCTTAA ACTTTCACTG TGCAAAAAGG GTCTTTAACT AAACCCCTTT ATATTTGAAG
                                                                       4920
     AGGGTCTTAT GGGTCCGCAG GAGAGACTCC AGGTCCTCCT TTTTCCGTAG TTCATATTCA
                                                                       4980
     AACTTCAGAT GCTCTTCTTT CTGATTGTCC TTCTACGAAA GTTCAAGAGA CGAGGGGAGG
                                                                      5040
     ATTTCGATAC GTAAAAATAT TCTGGTACCC TGAAAACGAC CGAAATCTAG AGAAACACTT
                                                                      5100
     CCTTGGAATG AAGACACCAC ACTGTATTAA CCTGTTTTGAT GGATGTCTCT AAATTTCGAG
                                                                       5160
     ATTCCATTTA TATTTTAAAA ATTCACATAT TACACAATTT GATGACTAAG ATTAACAAAC
                                                                      5220
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TCCCAATAAC AGAGTACTCG CCTATGTATA AACTTACATA AATCTTTTTA TTTGTTTATC
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- (2) INFORMATION FOR SEQ ID NO:29:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7874 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

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				TTGGTAGAGG		·1260
				CCGAGCCGGG		1320
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AGCAAGCCGA CGCCGCTCGC: CATAGTCGAG TGAGTTTCCG CCATTATGCC AATAGGTGTC # 5040 AND ADDRESS TO THE RESERVED
CATTTTTCCG GCGCAACGAC CGCAAAAAGG TATCCGAGGC GGGGGGACTG CTCGTAGTGT 5160
THE PART AGCT CAGT CACTO TOCACCOCTT TGGGCTGTCC TGATATTTCT ATGGTCCGCA 5220 525
       AAGGGGGACC TTCGAGGGAG CACGCGAGAG GACAAGGCTG GGACGGCGAA TGGCCTATGG ____5280
THE REPORT OF ACAGGCGGAA AGAGGGAAGC CCTTCGCACC GCGAAAGAGT TACGAGTGCG ACATCCATAG: 5340 18 02 12 12 12 12 12 12
5460
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